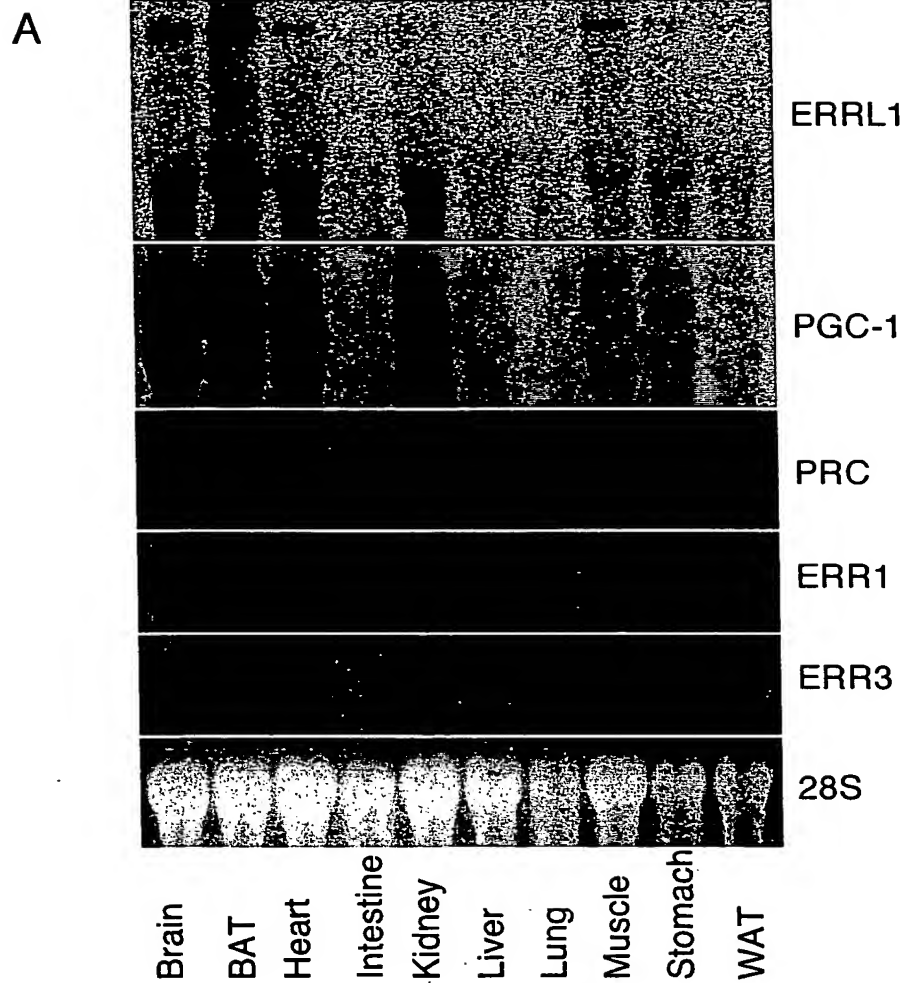


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Fig. 1

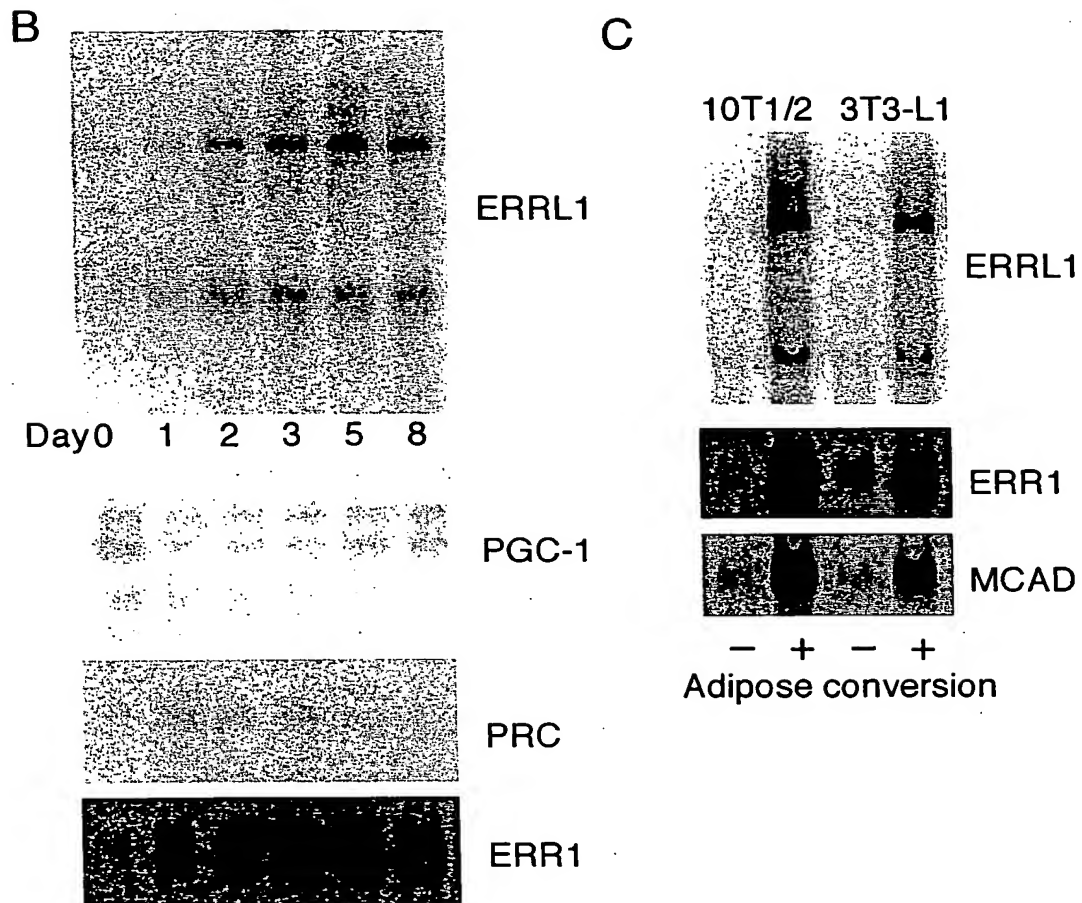
ERRL1	MAGNDCGALLDEELSSFFLNYSLTQGGDSGEEQ-LCADLPELDLSQLDASDFDSATCFG	59
PGC-1	MAWDMCSQDSVWSIDIECAALVGEDQPLCPDLPELDLSELVDNDLDTDSFLG	51
	*** ** *	
ERRL1	ELQWCPETSETEPSQYSPDDSELFQ-IDSENEA-LLAALTKTLDDIPEDDVGLAAFPELD	117
PGC-1	GLKWCSDQSEIISNQYNNEPANIFEKIDEENEANLLAVLTETLDSLVPDEGLPSFDALT	111
	* ** ** *	
ERRL1	EGDTPSCTPASAPLSAPPSPPTLERLLSPASDVDELSSLLQKLLLATSSPTASSDALKDGA	177
PGC-1	DGAVTTDNEASPSSM---PDGT-----PPPQEAEEPSLLKLLAPANTQLSYNECSGLS	163
	* *** *	
ERRL1	TWSQTSLS---RSQRPCVKVDGTQDKKPTTL---RAQSRPCTELHKHLTSVLP CPRVK	230
PGC-1	TQNHAANHTRIRTNPAIVKTENSWSNKAKSICQQKQRRPCSELLKYLTINDDPHTK	223
	* * ** *	
ERRL1	ACSPTPHPSRLLSKEE-----EEEVGEDCPSPW---LTPASPQDSLAQDTASPD SAQPP	282
PGC-1	PTENRNSSRDKASKKKSHTQPQSQHAQAKPTTSLPLTPESPNDP-----KGSPFEN---	276
	** * ** *	
ERRL1	EEDVRAMVQLIRYMHTYCLPQRKLPQRAPEPIQACSSLSRQVQPRSRHPPKAFWTEFSI	342
PGC-1	-----	
ERRL1	LRELLAQDILCDVSKPYRLAIPVYASLT PQSRPRPPKDSQASPAHSAMAEVRITASPKS	402
PGC-1	-----	
ERRL1	TGPRPSLRPLRLEVKRDVNKPTRQKREDEEEEEEEEEEEEEEEEEEWGRKRPGRGLP	462
PGC-1	-----	
ERRL1	WTKLGRKMDSSVCPVRRSRRLNPELGPWLTF TDEPLGALPSMCLDTETHNLEEDLGSLTD	522
PGC-1	-----	
ERRL1	SSQGRQLPQGSQIPALES PCESGCGD TDED PSCPQPTSRDSSRCLMLALSQSDSLGKXSF	582
PGC-1	-----KTI	279
	*	
ERRL1	EESLTVELCGTAGLTPPTTPPYKPM EEDPFKPDTKLSPGQDTAPSLPSPEAL--PLTATP	640
PGC-1	ERTLSVELSGTAGLTPPTTPPHKANQDNPFKASP KLPCKTVVPPPTKRARYSECSGTQ	339
	* * *** ** *	
ERRL1	GASHKLPRKHPERSEILSHLQHAT--TQVVSQAGQKRPFCSCSFGDHDYCOVL RPEAALQR	698
PGC-1	G-SHST-KKGPEQSEIYAQLSKSSGLSRGHEERKTRPSLR LFGDHDYCOQLNSKTDILI	397
	* ** * ** *	
ERRL1	KV---LRSWEPIGVHLEDLAQQGAPLPTETKAP---RR--EANQNCDP THKDSMQLRDHE	750
PGC-1	NISQELQDSRQLDFKDASCDWQGHICSS TDSGCYLRETLEASKQVSPCSTRK-QLQDQE	456
	* ** *	
ERRL1	IRASLTKHFG LLETALEGEDLASCKSPEYDTVFEDSSSS-----SGES-SFLL EEEEE	802
PGC-1	IRAE LNKHFHGHCQAVF-DDKSDKTSEL RDGDFSNEQFSKLPVF INSGLAM DGLFDDSED	515
	*** * ** *	
ERRL1	EEEGGEEDDEGEDS-----GVSPPCSD-HCPYQ---SPP---SKASRQLCSRSRSSSGSS	850
PGC-1	ESDKLSYPWDGTQPYSLFDVSPSCSSFN SPCRDVSPPKSLFSQRPQMRSRSRSESRHR	575
	* * ** *	
ERRL1	SCS-----SWSPATRKN-----FRRESRGPCS-----DG	874
PGC-1	SCSRSPYSRSPSRSPGSRSSSRSCY YESSHYRHRTHRNSPLYVRSRSPYSRRPRYDS	635
	*** * ** *	
ERRL1	TPSVRHAR-----KRRE---KAIGEGRVVYIRNLSSDMSSRELKKR	912
PGC-1	YEAYEHERLKRDEYRKEHEKRESERAKOREROKQKAIERRVYVVGKIRPDTTRTELDR	695
	* * * ** *	
ERRL1	FEVFGIEVCQVLT RSKRGQKHGFITFR--CSEHAALSVRNGATLRKRNEPSFHL SYGGL	970
PGC-1	FEVFGIEIECTVNL RDD-GDSYGFITYRYTCD AFAAL--ENGYTLRRSNETDFELYFCGR	752
	***** ** *	
ERRL1	RHFRWPRYTDYDPTSEESLPSSGKSKYEAMDFD SLLKEAQOSLH	1014
PGC-1	KQFFKS NYADLDTNSDDFD PASTKSKYDSLDFD SLLKEAQRSLRR	797
	* * ** *	

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F i g . 2



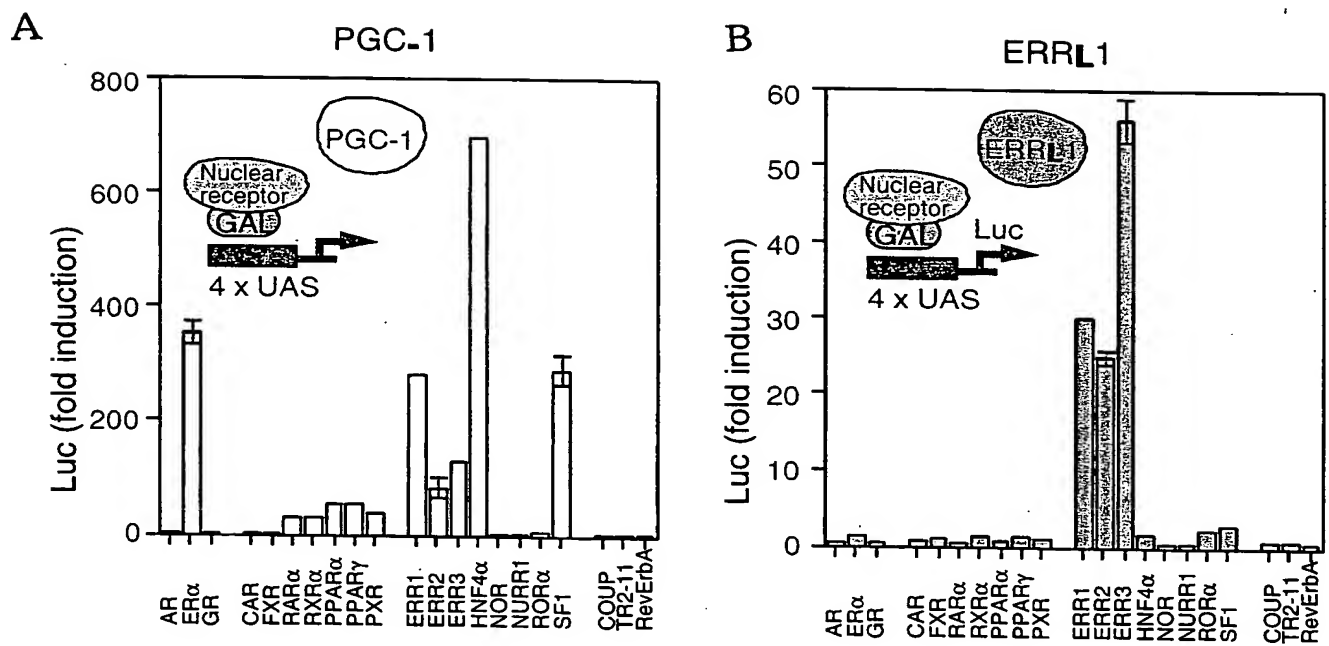
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Fig. 2



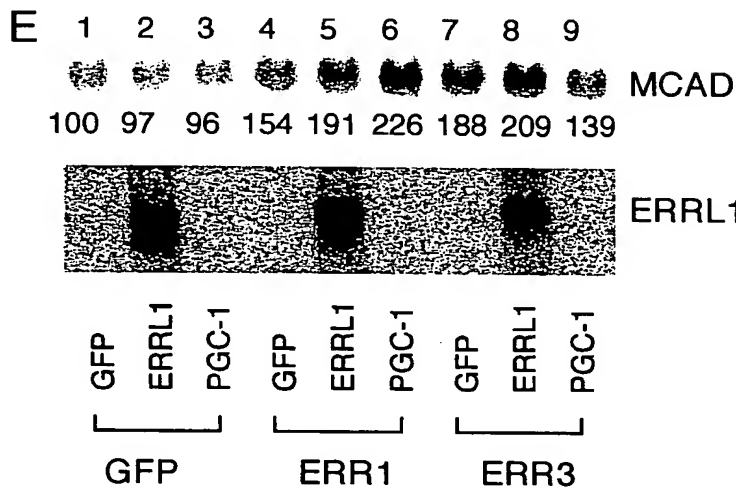
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Fig. 3

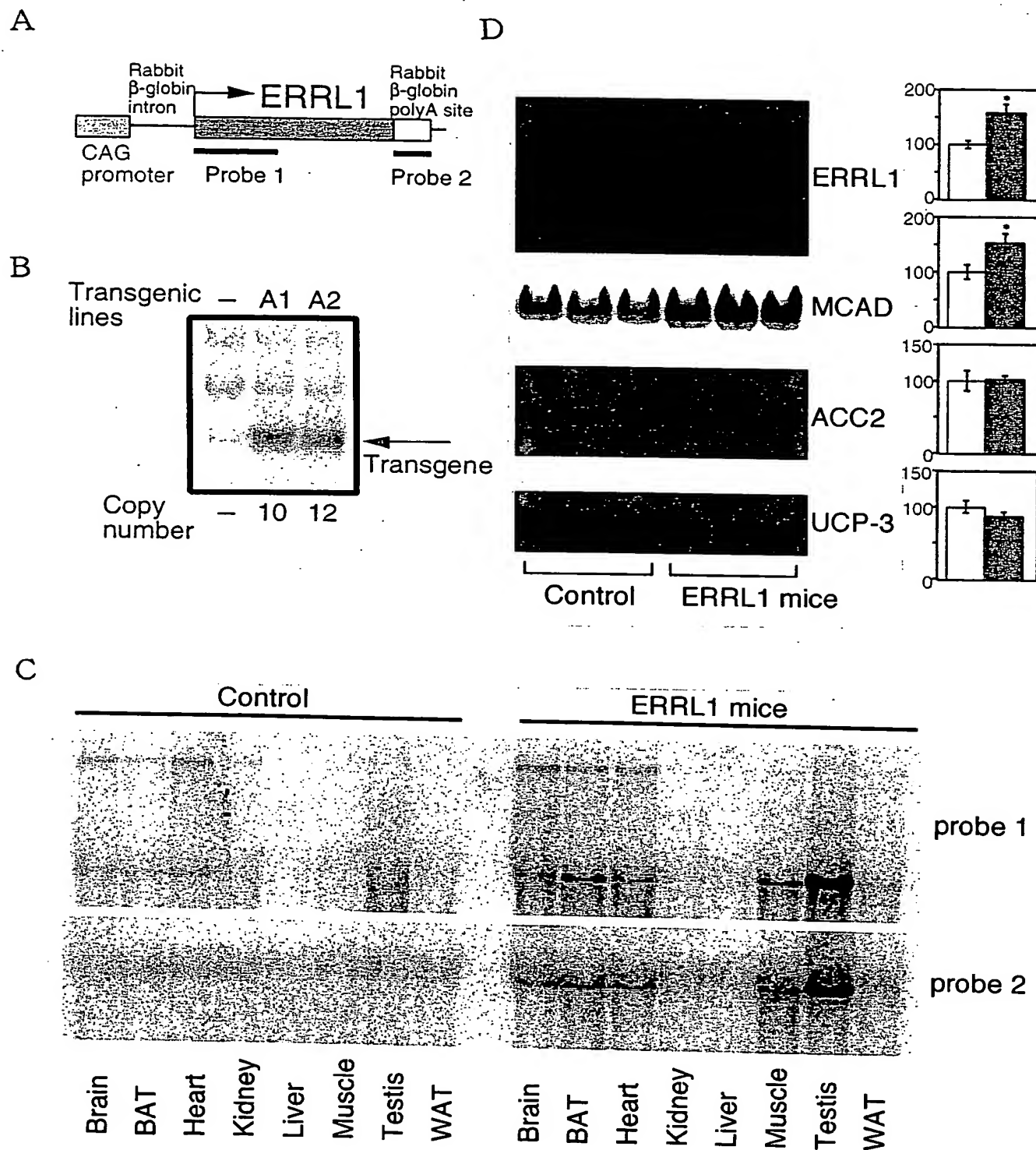


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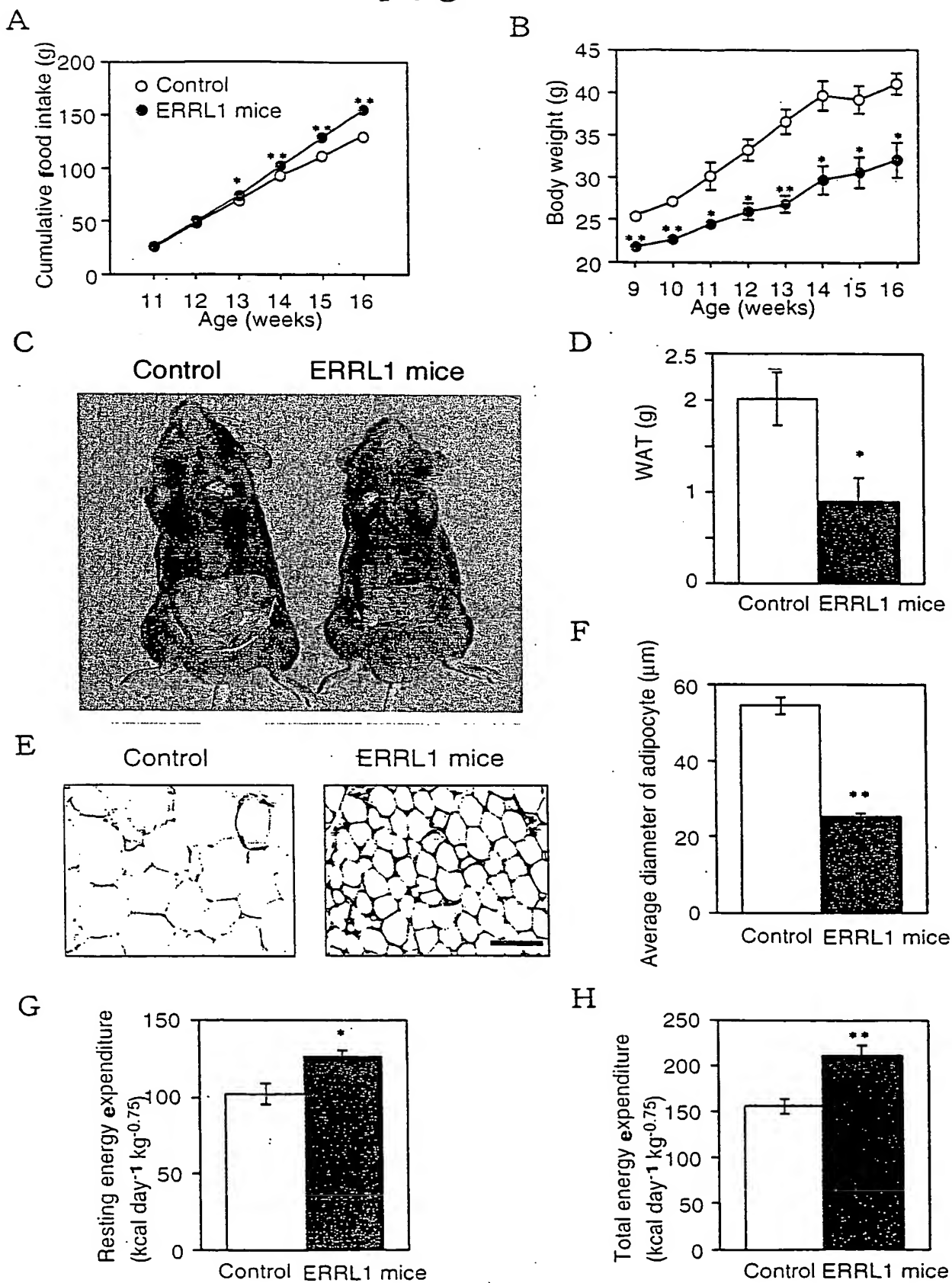


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Fig. 4



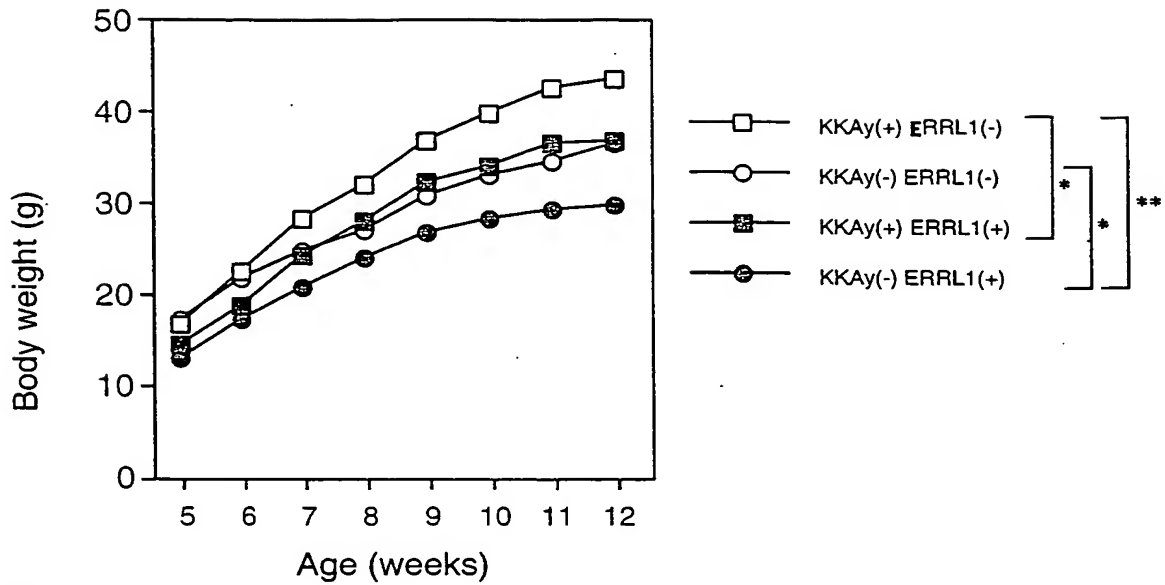
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Fig. 5



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Fig. 6

A



B

